AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph beginning at page 4, line 19, as follows:

As used herein, the term "sequence identity" or "percent identical" as applied to nucleic acid molecules is the percentage of nucleic acid residues in a candidate nucleic acid molecule sequence that are identical with a subject nucleic acid molecule sequence (such as the nucleic acid molecule sequence set forth in SEQ ID NO:3), after aligning the sequences to achieve the maximum percent identity, and not considering any nucleic acid residue substitutions as part of the sequence identity. No gaps are introduced into the candidate nucleic acid sequence in order to achieve the best alignment. Nucleic acid sequence identity can be determined in the following manner. The subject polynucleotide molecule sequence is used to search a nucleic acid sequence database, such as the ~~Genbank~~ GENBANK database, using the program BLASTN version 2.1 (based on Altschul et al., *Nucleic Acids Research 25*:3389-3402 (1997)). The program is used in the ungapped mode. Default filtering is used to remove sequence homologies due to regions of low complexity as defined in Wootton, J.C. and S. Federhen, *Methods in Enzymology 266*:554-571 (1996). The default parameters of BLASTN are utilized.

Please amend the paragraph beginning at page 5, line 1, as follows:

As used herein, the term "genetic mutation" is an alteration of the wild-type protein kinase C gamma (PRKCG) sequence deposited in ~~GenBank~~ GENBANK, provided as SEQ ID NO:3 that is not a recognized polymorphism (i.e., has a population frequency less than 1% in mammalian control subjects of the same species that do not exhibit ataxia).

Please amend the paragraph beginning at page 6, line 6, as follows:

The PRKCG human gene encompasses 24 kilobases and consists of 18 exons. The PRKCG cDNA coding sequence is provided herein as SEQ ID NO:1 which corresponds to nucleotides 187-2280 of ~~GenBank~~ GENBANK accession number NM_002739. Disclosed herein are nucleic acid mutations numbered sequentially with respect to the first nucleotide of SEQ ID NO:1. The PKCγ protein encoded by SEQ ID NO:1 is provided herein as SEQ ID NO:2. Disclosed herein are amino acid mutations numbered sequentially with respect to the first amino acid residue of SEQ ID NO:2. The entire 25 kilobase genomic locus that encompasses the

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PRKCG gene is provided herein as SEQ ID NO:3. With respect to the first nucleotide in SEQ ID NO:3, the 18 exons are as follows: exon 1: nucleotides 440 to 609; exon 2: nucleotides 1108 to 1139; exon 3: 2106 to 2188; exon 4: nucleotides 7583 to 7694; exon 5: nucleotides 7831 to 7962; exon 6: nucleotides 9619 to 9775; exon 7: nucleotides 10454 to 10588; exon 8: nucleotides 10933 to 11020; exon 9: nucleotides 11307 to 11336; exon 10: nucleotides 15904 to 16056; exon 11: nucleotides 16385 to 16573; exon 12: nucleotides 18178 to 18269; exon 13: nucleotides 18364 to 18426; exon 14: nucleotides 18556 to 18694; exon 15: nucleotides 21018 to 21098; exon 16: nucleotides 22580 to 22687; exon 17: nucleotides 24262 to 24402; and exon 18: nucleotides 24652 to 24840.

Please amend the paragraph beginning at page 11, line 1, as follows:

Once the nucleic acid sequence from the test subject is obtained, the sequence is compared to the nucleic acid sequence of one or more subjects not exhibiting ataxia in order to identify genetic mutations that are associated with ataxia. For example, resulting sequences can be aligned with the known exon sequence using a multiple sequence alignment tool, ~~Sequencher~~ SEQUENCHER (Gene Codes Corporation, Ann Arbor, MI), in order to identify any nucleotide changes as described in Example 4. In one embodiment, the information and analysis can be recorded on a database and the comparisons can be performed by a computer system accessing said database. In this manner, the amplified sequences of PRKCG from a subject exhibiting ataxia are sequenced until a mutation associated with ataxia is identified.

Please amend the paragraph beginning at page 11, line 11, as follows:

A mutation associated with ataxia encompasses any alteration of the wild-type protein kinase C gamma (PRKCG) sequence deposited in ~~GenBank~~ GENBANK, provided as SEQ ID NO:3, that is not a recognized polymorphism (i.e., has a population frequency less than 1% in mammalian control subjects of the same species that do not exhibit ataxia). A genetic mutation may be any form of sequence alteration including a deletion, insertion, point mutation or DNA rearrangement in the coding or noncoding regions. Deletions may be small or large and may be of the entire gene or of only a portion of the gene. Point mutations may result in stop codons, frameshift mutations or amino acid substitutions. Point mutations may also occur in regulatory

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regions, such as in the promoter of the PRKCG gene, leading to loss or diminution of expression of the mRNA. Point mutations may also abolish proper RNA processing, leading to loss of expression of the PRKCG gene product, or to a decrease in mRNA stability or translation efficiency. DNA rearrangements include a simple inversion of a single segment of DNA, a reciprocal or nonreciprocal translocation disrupting any portion of the gene, or a more complex rearrangement. The following characteristics are supportive, but are not required for a genetic mutation to be a causative mutation for ataxic neurological disease: 1) the change results in an amino acid substitution in a highly evolutionarily conserved residue; 2) the change occurs in a functional domain; 3) the change is predicted to affect splicing; or 4) the change cosegregates with disease in a family (where applicable).

Please amend the paragraph beginning at page 24, line 22, as follows:

Direct DNA sequencing of the PCR Fragments: 5 µl of PCR product from each sample confirmed to have a single correctly sized band was treated with 1 µl of ExoSAP-IT (US Biochemical, Cleveland, OH) at 37°C for 2 hours followed by heat inactivation at 85°C for 10 minutes. Direct DNA sequencing of the purified fragments was carried out by using a ~~BigDye~~ BIGDYE Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems Inc., Foster City, CA). The primers used for sequencing are listed in TABLE 2. For initial mutation screening, either forward or reverse primer was used. The PCR reaction contained 3 µl of treated PCR product (~100ng), 3 pmol primer, 1 µl sequencing buffer and 2 µl of ~~BigDye~~ BIGDYE reagent in a total volume of 10 µl. The sequencing reaction was carried out in a PTC-100 Programmable Thermal Controller (MJ Research Inc., Waltham, MA) with cycle conditions of 96°C for 2 min., 30 cycles of 96°C for 15 sec., 50°C for 10 sec. and 60°C for 4 min. The sequencing product was purified by ethanol/EDTA precipitation, then electrophoresed on an ABI DNA Sequencer (Applied Biosystems Inc., Foster City, CA).

Please amend the paragraph beginning at page 25, line 4, as follows:

Evaluation of cosegregation of ataxia and genetic mutations: Radioisotope dideoxy sequencing using two bases (wild type C and mutant T) was performed to evaluate the cosegregation of ataxia and the mutations in AT08 and to screen normal controls for a possible

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polymorphism. The forward primer for exon 4 was end-labeled with [γ^{32}]P by the T4 kinase reaction and sequencing was performed with the ~~AmpliCycle~~ AMPLICYCLE Sequencing Kit (Applied Biosytems Inc.). The sequencing products were then electrophoresed at 50°C on 6% polyacrylamide gels containing 7M urea.

Please amend the paragraph beginning at page 29, line 10, as follows:

Data Analysis: The resulting sequences were aligned with the known exon sequence using a multiple sequence alignment tool, ~~Sequencher~~ SEQUENCHER (Gene Codes Corporation, Ann Arbor, MI), in order to identify any nucleotide changes. Electropherograms were also visually examined to detect heterozygous base changes that might have been missed by ~~Sequencher~~ SEQUENCHER.

Please amend the paragraph beginning at page 30, line 1, as follows:

6. ~~BigDye~~ BIGDYE Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems Inc., Foster City, CA)

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